

Fig A. Sensitivity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 20M in each sample. Detections 2Mb away from critical region are reported.



Fig B. Specificity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 20M in each sample. Detections 2Mb away from critical region are reported.

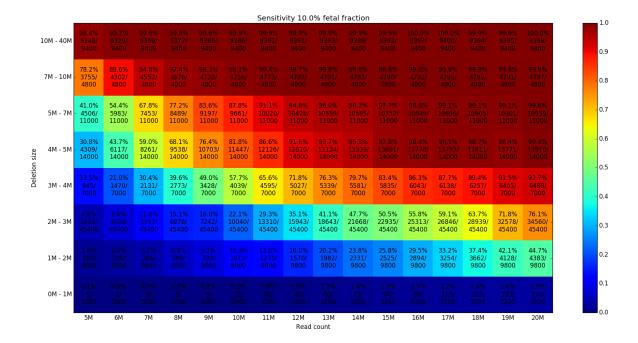


Fig C. Sensitivity of the prediction for different read count and microdeletion size.

Fetal fraction was set to 10% for all samples. Detections 2Mb away from critical region are reported.



Fig D. Specificity of the prediction for different read count and microdeletion size.

Fetal fraction was set to 10% for all samples. Detections 2Mb away from critical region are reported.

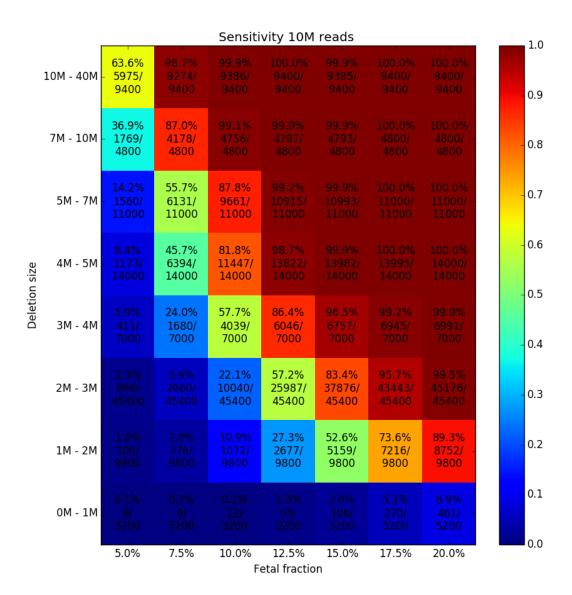


Fig E. Sensitivity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 10M in each sample. Detections 2Mb away from critical region are reported.

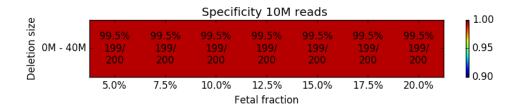


Fig F. Specificity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 10M in each sample. Detections 2Mb away from critical region are reported.

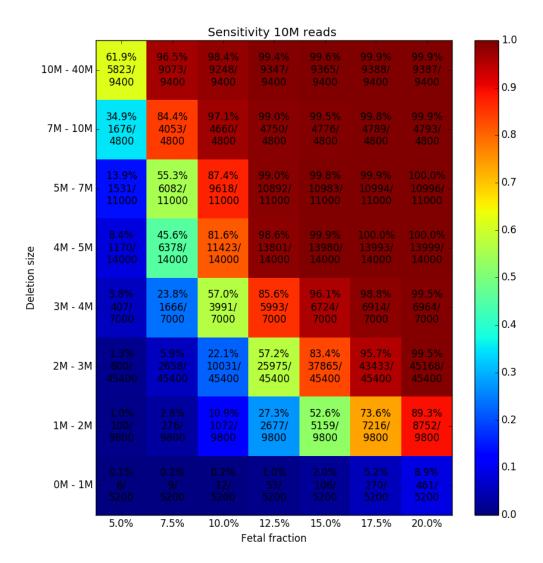


Fig G. Sensitivity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 10M in each sample. Detections 2Mb away from critical region are NOT reported.

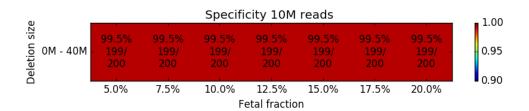
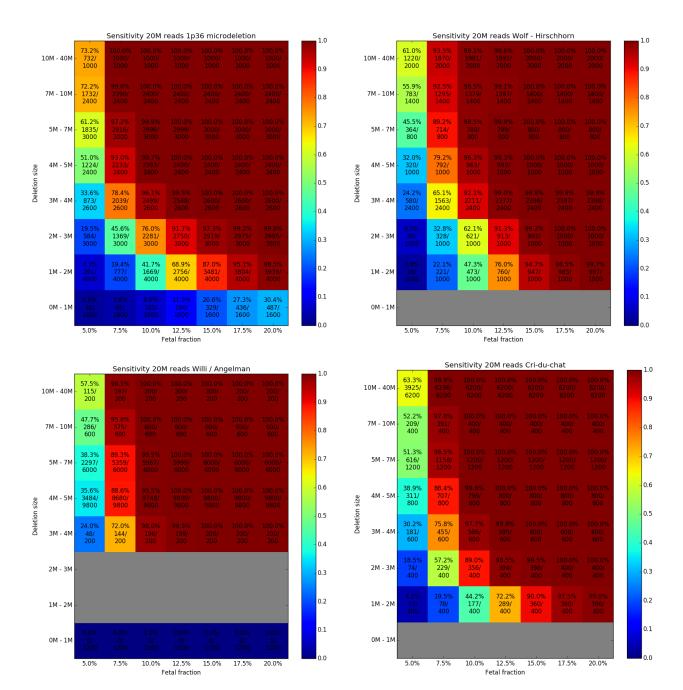


Fig H. Specificity of the prediction for different fetal fraction and microdeletion size.

Read count was set to 10M in each sample. Detections 2Mb away from critical region are NOT reported.



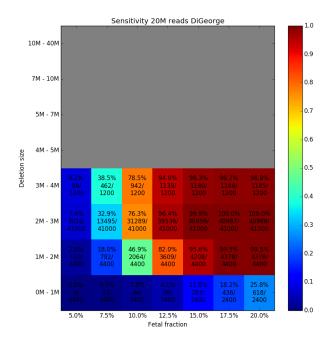


Fig I. Sensitivity of the prediction for different fetal fraction and size of microdeletion for different syndromes.

Read count was set to 20M in each sample. Detections 2M away from critical region are NOT reported.

						10	Eopsitivi	tv 10 09	6 fetal fr	action1r	36 micr	odolotio					
10	M - 40M	96.7% 967/ 1000	99.2% 99.2/ 1000	99.9% 999/ 1000	99.8% 998/ 1000	99.9% 999/ 1000	100.0% 1000/ 1000										
7	M - 10M	76.9% - 1846/ 2400	90.7% 2176/ 2400														
	5M - 7M	44.7% - 1340/ 3000	61.7% 1850/ 3000	76.1% 2282/ 3000	86.2% 2587/ 3000												
Deletion size	4M - 5M	31.2% - 750/ 2400	50.1% 1202/ 2400	67.4% 1617/ 2400	79.6% 1910/ 2400	87.9% 2109/ 2400											
	3M - 4M	10:8% 281/ 2600	19.9% 51.7/ 2600	32.1% 834/ 2600	44.0% 1145/ 2600	55.3% 1438/ 2600	67.6% 1757/ 2600	76.9% 2000/ 2600	83.5% 2172/ 2600	87.3% 2271/ 2600	90.1% 2343/ 2600						
	2M - 3M			16.9% 508/ 3000	23.0% 689/ 3000	30.2% 907/ 3000	38.4% 1153/ 3000	44.5% 1336/ 3000	49.5% 1484/ 3000	56.1% 1682/ 3000	59.2% 1777/ 3000	63.6% 1909/ 3000	66.3% 1988/ 3000	69.5% 2084/ 3000	71.7% 2151/ 3000	73.1% 2194/ 3000	76.0% 2281/ 3000
	1M - 2M				£8% 191/ 4000	7,7% 3087 4000	11.2% 448/ 4000	14.0% 560/ 4000	16.4% 656/ 4000	19,9% 797/ 4000	26.1% 1042/ 4000	27.7% 1107/ 4000	30.0% 1202/ 4000	32.8% 1313/ 4000	36.4% 1456/ 4000	39.0% 1561/ 4000	41.7% 1669/ 4000
	OM - 1M										3.4% 557 1600	5.7% 597 1600	4.0% 64/ 1600	5.1% 817 1600	5.6% 90/ 1600	5.8% 93/ 1600	6.6% 105/ 1600
		5M	6M	7M	8M	9М	10M	11M	12M Read	13M count	14M	15M	16M	17M	18M	19M	20M
							Sensitiv	ity 10.0	% fetal f	ractionV	Volf - Hir	schhorn					
10	М - 40М	90.3% 1806/ 2000				89.8% 1797/ 2000				93.3% 1866/ 2000							
7	M - 10M	80.6% - 1129/ 1400	87.8% 1229/ 1400	89.8% 1257/ 1400		90.6% 1268/ 1400											
	5M - 7M	54.5% - 436/ 800	66.5% 532/ 800	74.6% 597/ 800	81.0% 648/ 800	84.5% 676/ 800	88.0% 704/ 800	90.1% 721/ 800		91.9% 735/ 800							

0.9

0.6

0.3

0.2

0.9 0.8 0.7

0.5

0.4

0.3

0.1

1.0

0.8

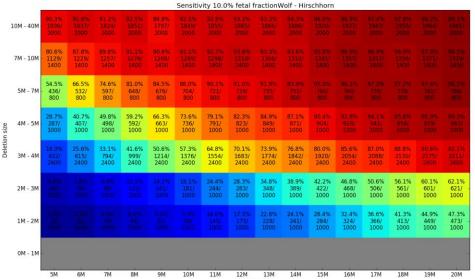
0.7

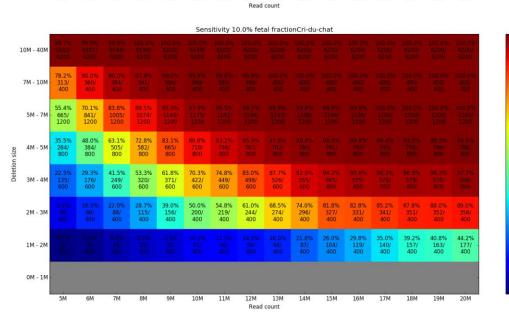
0.6

0.5

0.3

0.2





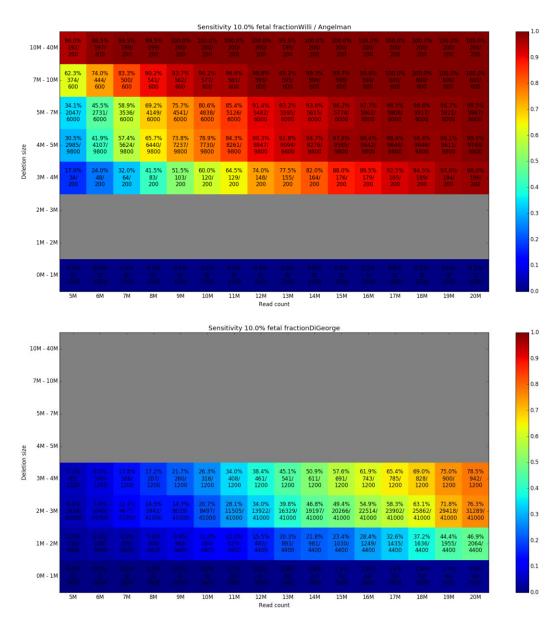


Fig J. Sensitivity of the prediction for different read count and microdeletion size.

Fetal fraction was set to 10% for all samples. Detections 2M away from critical region are NOT reported.

Table A. Detailed description of the control samples and their detection accuracy.

name	read count	fetal fraction	detection	local z score	size	syndrome
NA 17942	17.5M	4.15%	ND	ND	2.6M	DiGeorge
BA161216	25.27M	4.50%	ND/grey zone	-2,48	ЗМ	DiGeorge
NA22936	15.9M	4.86%	D	-5,28	21M	1p36 microdeletion
NA 14124	16.47M	5.11%	D	-8,35	17.7M	Cri-du-chat
BA34	19.24M	5.90%	ND	ND	0.9M	DiGeorge
NA09024	15.3M	7.30%	D	-4,82	5.3M	Willi / Angelman
NA09024	12.66M	7.60%	D	-5,79	5.3M	Willi / Angelman
NA 17942	19.6M	8.70%	D	-4,29	2.6M	DiGeorge
BA34	11 M	8.80%	ND	ND	0.9M	DiGeorge
NA00072	8.3M	9.10%	D	-16,98	9.3M	Wolf - Hirschhorn
NA22936	21.5M	9.85%	D	-10,66	21M	1p36 microdeletion
NA 11515	19.31M	10.60%	D	-5,59	6M	Willi / Angelman
BA34	9.9M	10%	ND	ND	0.9M	DiGeorge
BA161216	20.59M	11.20%	D	-4,71	ЗМ	DiGeorge
BA34	20.36M	11.50%	D	-5,34	0.9M	DiGeorge
BA34	8.9M	11.99%	D	-5,74	0.9M	DiGeorge
NA 11515	16.79M	12.20%	D	-9,02	6M	Willi / Angelman
NA09024	24.3M	13.40%	D	-7,38	5.3M	Willi / Angelman
NA 11515	15.71M	13.90%	D	-9,54	6M	Willi / Angelman
NA00072	8.4M	14.10%	D	-14,62	9.3M	Wolf - Hirschhorn
NA09024	15.37M	14.50%	D	-10.25/-5.58	5.3M	Willi / Angelman
NA 11515	19.26M	14.60%	D	-7,72	6M	Willi / Angelman
NA00072	16.2M	16.40%	D	-14,3	9.3M	Wolf - Hirschhorn
NA 17942	14.5M	16.69%	D	-7, 11	2.6M	DiGeorge
BA34	21.52M	17.30%	D	-6,52	0.9M	DiGeorge
NA 17942	19.45M	17.30%	D	-6,71	2.6M	DiGeorge
BA161216	20.39M	20.10%	D	-8,27	ЗМ	DiGeorge
NA 17942	20.39M	20.10%	D	-8,27	2.6M	DiGeorge
NA09024	16.1M	20.50%	D	-13.50/-5.71	5.3M	Willi / Angelman

Table B. The number, mean size of pathogenic regions, and resulting critical regions, as reported by our study and DECIPHER database.

The number of pathogenic regions overlapping its corresponding critical region is reported in brackets. Finally, the number of pathogenic deletions from DECIPHER database that does not overlap ISCA database is low.

Identifi	ication of a syndrome	Number of path	ogenic deletions	Mean size of pathogenic deletions			
Band	Name	ISCA	DECIPHER	ISCA	DECIPHER		
1p36	1p36 deletion	102 (100)	54 (52)	4,131,271	3,174,263		
4p16.3	Wolf-Hirschhorn	48 (48)	27 (27)	6,713,778	4,819,991		
5p15	Cri-du-chat	50 (50)	24 (24)	14,887,247	8,873,724		
15q11	Angelman / Prader-Willi	90 (90)	133 (133)	5,061,279	2,534,265		
22q11.21	DiGeorge	280 (245)	136 (120)	2,368,692	2,444,038		

Critical	Pathogenic deletions from			
ISCA	DECIPHER	DECIPHER not in ISCA critical region		
chr1: 564,424 - 21,598,492	chr1: 120,840 - 22,542,549	3		
chr4: 85,040 - 2,010,761	chr4: 71,552 - 5,506,588	2		
chr5: 1 - 15,678,560	chr5: 113,576 - 18,992,827	2		
chr15: 22,779,922 - 28,559,437	chr15: 22,373,311 - 28,560,803	2		
chr22: 18,661,724 - 21,505,417	chr22: 18,890,162 - 21,464,119	15		